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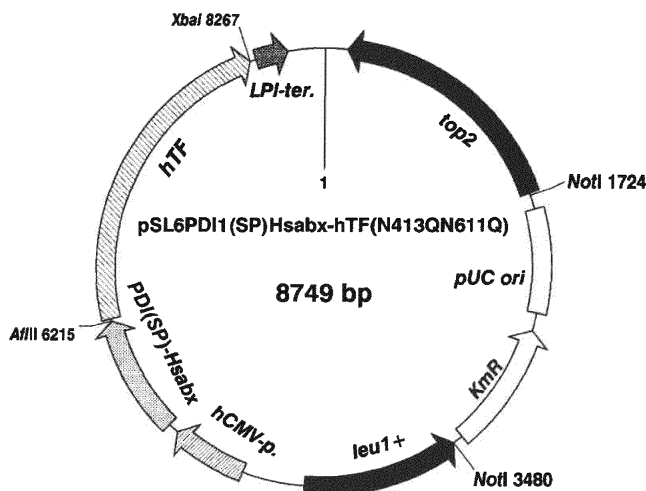
(54) **TRANSFORMANT, AND TRANSFERRIN MANUFACTURING METHOD**

(57) To provide a method for producing transferrin by secretion with high productivity using a transformant of *Schizosaccharomyces pombe*, and a transformant suitable for the method.

A transformant using *Schizosaccharomyces pombe* as a host, comprising a transferrin gene and a secretion signal peptide gene expressing transferrin to which a se-

cretion signal peptide which functions in the host binds, located in an upstream region of the transferrin gene, and having Gas2 gene endogenous to the host deleted or inactivated; and a method for producing transferrin, which comprises culturing the transformant in a liquid medium and obtaining transferrin from the liquid medium.

Fig. 1



## Description

## TECHNICAL FIELD

5 [0001] The present invention relates to a method for producing transferrin by using a transformant from *Schizosaccharomyces pombe* (hereinafter referred to as "*S. pombe*") as a host and having a transferrin gene integrated thereinto.

## BACKGROUND ART

10 [0002] Transferrin (hereinafter sometimes referred to as "TF") is one of glycoproteins which bind to  $\text{Fe}^{3+}$  ions and is deeply involved in iron metabolism. Particularly human serum transferrin (hereinafter sometimes referred to as "human transferrin" or "hTF") belongs to a family of iron-binding proteins in a human body, is involved in iron transport/metabolism in the body and is used as additives to be used for a medium for animal cell culture, a pharmaceutical preparation or a DDS carrier. TF is an about 80 kDa glycoprotein having two domains named N-lobe and C-lobe, and it is synthesized  
15 by translation as an immature protein having a secretion signal peptide at its N-terminal and is then secreted out of the cell as a mature glycoprotein having the secretion signal peptide cleaved.

[0003] As the most common method for TF production, a method for producing a full-length recombinant protein by using a cell line of mammal cells such as baby hamster kidney cells (BHK cells) has been known. Further, a method of using budding yeast *S. pombe* has been known. *S. pombe* has, as different from budding yeast *Saccharomyces cerevisiae*, cell division and transcription forms close to those of human cells and contains no substance which has adverse effects on the body. Accordingly, the method for producing TF full-length recombinant protein employing *S. pombe* is excellent as a method for producing TF to be administered to human, such as a pharmaceutical preparation. For example, Patent Document 1 discloses a method such that a transformant using *S. pombe* as a host and having a *hTF* gene introduced is cultured in a liquid medium containing casamino acids to efficiently produce hTF, which is made to be  
25 secreted to the liquid medium and recovered.

[0004] On the other hand, in a heterologous protein production system employing an eukaryotic microorganism such as a yeast, in order to improve the efficiency for production of the desired heterologous protein, it has been known to use an improved host having a part of or the entire genome portion of a host unnecessary or disadvantageous for heterologous protein production eliminated or inactivated. For example, Patent Document 2 discloses that use of an improved host having at least one gene selected from genes encoding a specific protease (protease gene group) of *S. pombe* eliminated or inactivated, improves the efficiency for production of a heterologous protein.  
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[0005] Further, hTF protein can be secreted and produced by production in a state where a secretion signal (endoplasmic reticulum targeting signal) peptide is added to the N-terminal of hTF protein. For example, by culturing a transformant of *S. pombe* which has introduced a structural gene encoding a fusion protein having a secretion signal peptide recognized by *S. pombe*, such as a polypeptide derived from secretion signal of a precursor of a mating pheromone (P-factor) relating to mating of *S. pombe*, fused to the N-terminal of hTF protein, from the produced fusion protein, secretion signal peptide is removed in the Golgi apparatus or the endoplasmic reticulum, and hTF protein is secreted into the medium. For example, Patent Document 3 discloses that by expressing, at the N-terminal side of the desired foreign protein, a partial protein composed of a secretion signal peptide of PDI1 (protein disulfide isomerase 1) which is a protein  
35 having a molecular chaperone function and localized in the endoplasmic reticulum, an a-domain, a b-domain and an x-domain, or a partial protein composed of an endoplasmic reticulum targeting signal peptide of PDI1, an a-domain, a b-domain, a b'-domain and an x-domain, in a fused state, the amount of secretory production of the foreign protein by *S. pombe* can be increased. PDI1 comprises, from the N-terminal, an ER targeting signal, a-domain, b-domain, b'-domain, x-domain, a'-domain and c-domain containing an ER retention signal (ADEL), in this order. Each of the a-domain and the a'-domain has one active site (CGHC) for molecular chaperone activity. All the four domains a, b, b' and a' form a thioredoxin fold.  
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## PRIOR ART DOCUMENTS

50 PATENT DOCUMENTS

## [0006]

Patent Document 1: JP-A-2011-125281  
55 Patent Document 2: WO2007/015470  
Patent Document 3: WO2013/111754

## DISCLOSURE OF INVENTION

## TECHNICAL FIELD

5 **[0007]** The object of the present invention is to provide a method for producing TF by secretion with high productivity using a transformant of *S. pombe*, and a transformant suitable for the method.

## SOLUTION TO PROBLEM

10 **[0008]** The transformant of the present invention is a transformant using *S. pombe* as a host, comprising a *TF* gene and a secretion signal peptide gene expressing TF to which a secretion signal peptide which functions in the host binds, located in an upstream region of the *TF* gene, and having *Gas2* gene endogenous to the host deleted or inactivated.

**[0009]** The transformant is preferably such that the *TF* gene is a gene encoding human transferrin.

15 **[0010]** Further, the transformant is preferably such that the *TF* gene is a mutant *TF* gene having a mutation introduced to a gene encoding natural mammal TF, and the mutant *TF* gene is a gene encoding mutant TF having at least one aspartic residue which is an N-linked glycosylated portion of natural TF deleted or substituted with another amino acid residue.

**[0011]** Further, the transformant is preferably such that at least one protease gene endogenous to the host is deleted or inactivated. The protease gene is preferably a gene selected from the group consisting of a metalloproteinase gene group, a serine protease gene group, a cysteine protease gene group and an aspartic protease gene group. The protease gene to be deleted or inactivated is preferably at least one gene selected from the group consisting of *psp3* gene, *isp6* gene, *ppp53* gene, *ppp16* gene, *ppp22* gene, *sxa2* gene, *ppp80* gene and *ppp20* gene.

20 **[0012]** The transformant is preferably such that the *TF* gene is located downstream of a gene encoding a secretory carrier protein containing a secretion signal peptide, directly or indirectly, and more preferably such that the gene encoding a secretory carrier protein is a fusion gene of a gene encoding a secretion signal peptide portion of host PDI1, a gene encoding an ab-domain portion of human PDI1, and a gene encoding an x-domain portion of host PDI1.

25 **[0013]** The method for producing TF of the present invention comprises culturing the transformant of the present invention in a liquid medium and obtaining transferrin from the liquid medium.

**[0014]** The method for producing TF is preferably such that the transformant is cultured in a liquid medium having a pH of from 5.5 to 6.5, preferably such that the transformant is cultured in a liquid medium containing adenine, and also preferably such that the transformant is cultured until the cell-density ( $OD_{660}$ ) reaches 100 or higher, and then transferrin is obtained from the liquid medium.

30 **[0015]** The method for producing a transformant of the present invention comprises integrating into *S. pombe* as a host, a secretion signal peptide gene which functions in the host, and a *TF* gene located downstream of the secretion signal peptide gene, and deleting or inactivating *Gas2* gene endogenous to the host.

## ADVANTAGEOUS EFFECTS OF INVENTION

**[0016]** By culturing the transformant of the present invention, TF can be produced efficiently.

40 **[0017]** Further, according to the method for producing TF of the present invention, TF can be produced by secretion with high productivity using *S. pombe*.

## BRIEF DESCRIPTION OF DRAWINGS

45 **[0018]**

Fig. 1 is a diagram illustrating the structure of secretory expression vector pSL6PDI1(SP)Hsabx-hTF(N413QN611Q).

Fig. 2 is a CBB stained image of culture broths of A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain after SDS-PAGE.

50 Fig. 3 is a graph illustrating changes with time of the secretion amounts of hTF(N413Q/N611Q) protein from A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain.

Fig. 4 is CBB stained images of fractions of hTF(N413Q/N611Q) protein in culture supernatants of A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain, purified by DEAE chromatography, after SDS-PAGE.

## DESCRIPTION OF EMBODIMENTS

55 [*TF* gene, secretion signal peptide gene]

**[0019]** In the present invention, "*TF* gene" means a structural gene encoding mature TF protein. Further, the mature

TF protein will be hereinafter referred to as "TF protein".

**[0020]** In cells of a species to which the *TF* gene is endogenous, a fusion protein having a protein (secretory carrier protein) containing a secretion signal peptide and TF protein linked to each other, is expressed, and from the fusion protein, the secretory carrier protein is cleaved out in the endoplasmic reticulum or the Golgi apparatus, and the TF protein is secreted out of the cells.

**[0021]** On the other hand, since *TF* gene is exogenous to *S. pombe* as a host in the present invention, even when a fusion protein having a secretory carrier protein and TF protein linked to each other is expressed in the host, the secretory carrier protein is not necessarily cleaved out in the host cells. Accordingly, as the secretion signal peptide or the secretory carrier protein in the present invention is preferably a secretion signal peptide or a secretory carrier protein other than one endogenous to the host at its N-terminal side of TF protein, which sufficiently functions in the host. In the present invention, the term (a secretion signal peptide which) "functions in the host" means having a function to secrete the fusion protein expressed in the host out of the host cells as the TF protein.

**[0022]** Further, in the present invention, the TF protein and the secretion signal peptide or the secretory carrier protein may be directly linked to each other, or may be indirectly linked to each other by a linker composed of a peptide comprising one to several tens amino acid residues.

[Transformant]

**[0023]** The transformant of the present invention is a transformant using *S. pombe* as a host, comprising a *TF* gene and a secretion signal peptide gene expressing TF protein to which a secretion signal peptide which functions in the host binds, located in an upstream region of the *TF* gene, and having *Gas2* gene endogenous to the host deleted or inactivated.

**[0024]** The TF protein encoded by the *TF* gene which the transformant of the present invention has, may be a natural TF protein derived from any species (TF protein encoded by a *TF* gene present in the chromosome of a wild type organism) or may be a modified protein of a natural TF protein. The modified protein may, for example, be a polypeptide comprising an amino acid sequence of a natural TF protein, in which one or several amino acids are substituted, added or deleted, and having a TF function. A polypeptide comprising an amino acid sequence having an identity to the amino acid sequence of a natural TF protein of at least 80%, preferably at least 85%, more preferably at least 90%, further preferably at least 95%, and having a TF function, may be mentioned. The TF function means a function to bind to  $Fe^{3+}$  ions and to bind to the TF receptor on the cell surface to be incorporated into the cell. The TF protein encoded by the *TF* gene which the transformant of the present invention has, is preferably a natural TF protein derived from a mammal such as human, monkey, mouse, rat, rabbit, cattle, horse, dog, cat, etc., or a modified protein thereof, particularly preferably hTF or a modified protein thereof.

**[0025]** In a case where the TF protein encoded by the *TF* gene which the transformant of the present invention has, is a modified protein of a natural TF protein, the modification is, for example, preferably point mutation such that at least one aspartic acid residue as the N-linked glycosylated portion after translation, is deleted or substituted by another amino acid residue. In a case where a protein having a N-linked glycosylated portion is produced by secretion, the resulting recombinant protein is modified with a high mannose sugar chain having non-uniform length, and the uniformity or the quality may thereby be decreased.

**[0026]** In a case where the *TF* gene which the transformant of the present invention has, is a modified *TF* gene encoding a modified TF protein mutated to delete the N-linked glycosylated portion, by culturing such a transformant, a recombinant TF protein which has a stable TF function and which has a uniform quality can be produced by secretion. For example, such a modified *TF* gene is preferably a modified *TF* gene encoding a modified TF protein in which at least one aspartic acid residue as an N-linked glycosylated portion of the two N-linked glycosylated portions (432nd and 630th aspartic acid residues) of a natural hTF protein, is deleted or substituted with an amino acid residue other than an aspartic acid residue, more preferably a modified *TF* gene encoding a modified TF protein in which the two N-linked glycosylated portions are substituted with an amino acid residue other than an aspartic acid residue, further preferably a modified *TF* gene (SEQ ID NO: 2) encoding a mutant TF protein in which the two N-linked glycosylated portions are substituted with glutamine residue.

**[0027]** The secretion signal peptide gene which the transformant of the present invention has is a structural gene encoding a secretion signal peptide which functions in the transformant cell. The secretion signal peptide gene may be a part of a structural gene encoding a secretory carrier protein. That is, the structural gene encoding a secretory carrier protein may have a structural gene portion encoding a secretory carrier protein other than the secretion signal peptide gene portion, downstream the secretion signal peptide gene. The secretion signal peptide may be any peptide which functions in *S. pombe* and may, for example, be ones disclosed in WO1996/23890 such as a secretion signal peptide of a secretory protein endogenous to *S. pombe*, or P3 secretion signal (34th amino acid residue), and is preferably a secretion signal peptide of *S. pombe* PDI1.

**[0028]** The secretory carrier protein which functions in *S. pombe* is preferably a PDI1 full-length protein containing a

secretion signal peptide, a PDI1 partial protein, or a protein having such a modified protein fused. Particularly preferred is a protein containing a-domain of PDI1 or a protein containing a'-protein of PDI1, more preferably a protein containing at least one of a-domain and a'-domain and at least one of b-domain and b'-domain of PDI1, further preferably a protein containing at least one of a-domain and a'-domain, at least one of b-domain and b'-domain and x-domain of PDI1 (see Patent Document 3). All the respective domains of PDI1 contained in the protein fused downstream the secretion signal peptide may be derived from a single species, or they may be a combination of domains derived from two or more species.

**[0029]** In the transformant of the present invention, in order for more increased TF secretory production capability, the secretory carrier protein is preferably a fused gene having, in order from the upstream side, a secretion signal peptide gene of *S. pombe* PDI1 and a gene encoding abx-domain portion of human PDI1 or a gene encoding abb'-x-domain portion of human PDI1 directly or indirectly linked, or a fusion protein having a secretion signal peptide gene of *S. pombe* PDI1, a gene encoding ab-domain portion of human PDI1 or a gene encoding abb'-domain portion of human PDI1, and a gene encoding x-domain portion of *S. pombe* PDI1 directly or indirectly linked.

**[0030]** TF gene is exogenous to *S. pombe*. Accordingly, the transformant of the present invention is obtained by biogenetically introducing a TF gene derived from an organism other than *S. pombe*, into *S. pombe*. The nucleotide sequence of the TF gene which the transformant of the present invention has may be the gene sequence of the species from which the TF protein is derived as it is, or the gene sequence may be modified by changing its codons to ones frequently used in *S. pombe*.

**[0031]** The copy number of a gene having the secretion signal peptide gene and the TF gene directly or indirectly linked to each other of the transformant (hereinafter referred to as SP-TF gene) may be one or two or more. The SP-TF gene may be introduced as the plasmid as an extrachromosomal gene in *S. pombe*, or may be introduced into the plasmid of *S. pombe*. By introducing a foreign gene to the chromosome, a transformant excellent in the passage stability can be obtained.

**[0032]** Regarding the gene recombination method using yeast as a host, for more stably and efficiently expressing heterologous proteins, various expression systems, particularly an expression vector, a secretion signal, a gene introduction expression vector, etc. are developed, and for production of the transformant of the present invention, they are widely applicable. For example, as an expression system using *S. pombe* as a host, Japanese Patent No. 2776085, JP-A-H07-163373, JP-A-H10-215867, JP-A-H10-215867, JP-A-H11-192094, JP-A-H11-192094, JP-A-2000-262284, WO96/023890 etc. have been known, and for production of the transformant of the present invention, such expression systems are widely applicable.

**[0033]** Introduction of the SP-TF gene into *S. pombe* as a host is carried out, for example, by introducing an expression cassette containing the SP-TF gene, and a promoter and a terminate which function in *S. pombe* as it is into the host cell, or by introducing a vector having such a cassette integrated into the host cell. The expression cassette may contain at least one of a 5'-untranslation region and a 3'-untranslation region, and may contain an auxotrophic complementation marker such as *ura4* gene.

**[0034]** As the promoter which functions in *S. pombe*, a promoter endogenous to *S. pombe*, such as an alcohol dehydrogenase gene promoter, a *nmt1* gene promoter, a fructose 1,6-bisphosphatase gene promoter, an invertase gene promoter (WO99/23223) or a heat shock protein gene promoter (WO2007/26617, WO2014/030644), or a promoter derived from an animal cell virus such as a hCMV promoter or a SV40 promoter may, for example, be mentioned. As the terminator which functions in *S. pombe*, a LPI (human lipocortin I) terminator may, for example, be mentioned.

**[0035]** As the vector into which the expression cassette is integrated, a plasmid derived from *E. coli* such as pBR322, pBR325, pUC118, pUC119, pUC18, pUC19 or the like may suitably be used. The vector preferably has a marker to select the transformant. Such a marker may, for example, be *ura4* gene (an auxotrophic complementation marker) or isopropyl malate dehydrogenase gene (*leu1* gene).

**[0036]** In a case where an expression cassette containing the SP-TF gene is integrated into *S. pombe* chromosome by a homologous recombination method, the target site into which the expression cassette is integrated may be present in only one position of the *S. pombe* chromosome, or may be present in two or more positions. In a case where two or more target sites are present, the vector may be integrated into two or more positions in the *S. pombe* chromosome. When the expression cassette is integrated into one target site, the target site disclosed in JP-A-2000-262284 may, for example, be used. By using two or more types of vectors having different recombination regions, the vectors can be integrated into different target sites.

**[0037]** As the vector having an expression cassette containing the SP-TF gene integrated, a vector having a secretion signal peptide gene and a *hTF* gene integrated, disclosed in Patent Document 1, Patent Document 3 or the like may, for example, be used.

**[0038]** In the transformant of the present invention, Gas2 gene (SPBC29A10.08.1) endogenous to *S. pombe* as a host is deleted or inactivated. As shown in the following Examples, when a transformant of *S. pombe* having the SP-TF gene introduced is cultured at high density at a cell-density (optical density measured by a turbidimeter at 660 nm: OD<sub>660</sub>) of at least 100, the expression amount of Gas2 (1,3-β-glucanosyl transferase) protein, as well as TF, increases. Gas2 protein is a glycoprotein localizing in the cell wall and involved in the biosynthesis of the cell wall of fission yeast, and is

not considered to be directly involved in expression and secretion of TF. Nevertheless, in the high density cell culture process of TF expression strain (transformant having the *SP-TF* gene introduced), Gas2 protein as well as TF protein is secreted in a large amount into the liquid medium, and TF production efficiency decreases. Strangely, the increase of the expression and secretion amount of Gas protein observed at the time of high density culture of TF expression strain is not clearly observed at the time of common batch culture at OD<sub>660</sub> of from 20 to 30. Since Gas2 gene is deleted or inactivated in the transformant of the present invention, Gas2 protein is not expressed and the secretion amount of TF into the liquid medium increases, even at the time of the high density culture.

**[0039]** Further, the entire nucleotide sequence of the *S. pombe* chromosomes is stored and opened to the public in "*Schizosaccharomyces pombe* Gene DB (<http://www.genedb.org/genedb/pombe/>)" of Sanger Institute. The sequence data of *S. pombe* genes described in the present specification are available from the data base by searching with a gene name or a systematic name.

**[0040]** The transformant of the present invention is preferably one in which at least one type of protease gene (gene encoding protease) is deleted or inactivated. When the protease activity of at least one type of protease gene endogenous to *S. pombe* is deleted or inactivated in the transformant, TF protein production efficiency increases, and TF protein production amount more increases. The transformant of the present invention is preferably one in which at least one type of gene selected from the group consisting of a serine protease gene group (a group of genes encoding serine protease), an amino peptidase gene group (a group of genes encoding amino peptidase), a carboxypeptidase gene group (a group of genes encoding carboxypeptidase), and a dipeptidase gene group (a group of genes encoding dipeptidase) is deleted or inactivated.

**[0041]** The transformant of the present invention may be one in which only one type of protease gene is deleted or inactivated, or may be one in which two or more types of protease gene are deleted or inactivated. Among them, preferred is a transformant in which at least one type of gene selected from the group consisting of a metalloproteinase gene group (a group of genes encoding metalloproteinase), a serine protease gene group, a cysteine protease gene group (a group of genes encoding cysteine protease) and an aspartic protease gene group (a group of genes encoding aspartic protease) is deleted or inactivated, and also preferred is a transformant in which at least one type of gene selected from the group consisting of a metalloproteinase gene group and a serine protease gene group and at least one type of gene selected from the group consisting of a cysteine protease gene group and an aspartic protease gene group, are deleted or inactivated.

**[0042]** The four types of protease gene group of *S. pombe* may, for example, be as follows.

**[0043]** Metalloproteinase gene group: *cdh4*(SPAC23H4.09), *mas2*(SPBC18E5.12c), *pgp1*(SPCC1259.10), *ppp20*(SPAC4F10.02), *ppp22*(SPBC14C8.03), *ppp51*(SPAC22G7.01c), *ppp52*(SPBC18A7.01), *ppp53*(SPAP14E8.04).

**[0044]** Serine protease gene group: *isp6*(SPAC4A8.04), *ppp16*(SPBC1711.12), *psp3*(SPAC1006.01), *sxa2*(SPAC1296.03c).

**[0045]** Cysteine protease gene group: *ppp80*(SPAC19B12.08), *pca1*(SPCC1840.04), *cut1*(SPCC5E4.04), *gpi8*(SPCC11E10.02c).

**[0046]** Aspartic protease gene group: *sxa1*(SPAC26A3.01), *yps1*(SPCC1795.09), *ppp81*(SPAC25B8.17).

**[0047]** The transformant of the present invention may be produced by deleting or inactivating *Gas2* gene of the transformant having an expression cassette containing the *SP-TF* gene introduced into *S. pombe* as a host, and may also be produced by introducing an expression cassette containing the *SP-TF* gene into *S. pombe* having *Gas2* gene preliminarily deleted or inactivated. By using as a host a *S. pombe* mutant strain in which at least one type of protease gene is deleted or inactivated, a transformant into which the *SP-TF* gene is introduced, in which *Gas2* gene is deleted or inactivated, and in which at least one type of protease gene is deleted or inactivated, is obtained. The mutant strain in which at least one type of protease gene endogenous to *S. pombe* is deleted or inactivated may, for example, be preferably a *S. pombe* mutant strain in which *psp3* gene, *isp6* gene, *ppp53* gene, *ppp16* gene, *ppp22* gene, *sxa2* gene, *ppp80* gene and *ppp20* gene are deleted or inactivated, such as A8 strain as disclosed in Patent Document 2.

**[0048]** Deletion or inactivation of *Gas2* gene, and deletion or inactivation of protease gene may be carried out by publicly known methods. Specifically, the Latour system (Nucleic Acids Res. (2006) 34: e11, and WO2007/063919) can be used to delete the gene. Further, the gene may be inactivated by introducing mutation into a part of the gene by a mutant screening method using mutagens (Koubo Bunshi Idengaku Jikken-Hou, 1996, Japan Scientific Societies Press), random mutations using PCR (PCR Methods Application, 1992, vol. 2, p. 28-33) and the like. Further, the portion at which a specific gene is deleted or inactivated may be an ORF (open reading frame) portion or may be an expression control sequence. Particularly preferred is deletion or inactivation by substituting the ORF portion of structural gene by a marker gene by means of PCR-mediated homologous recombination (Yeast, vol. 15, pages 943 to 951, 1998).

**[0049]** As the transformation method, any known transformation method may be used. The transformation method may, for example, be a conventional method like lithium acetate method, electroporation method, spheroplast method, glass-beads method or the like, and a method disclosed in JP-A-2005-198612. Further, a commercially available yeast transformation kit may be used.

**[0050]** The transformant of the present invention may be cultivated in the same manner as a natural yeast of the genus

*Schizosaccharomyces*.

**[0051]** As a liquid medium for culturing the transformant, a known yeast culture medium may be used so long as it contains a carbon source, a nitrogen source, an inorganic salt, etc. which a yeast of the genus *Schizosaccharomyces* can utilize, and is capable of efficiently culturing a yeast of the genus *Schizosaccharomyces*. The liquid medium may be a natural medium or a synthetic medium.

**[0052]** The liquid medium may, for example, be MMA (Minimal medium with agar), SDC (Synthetic dextrose complete medium), TES (0.5% Bacto-yeast extract, 3% glucose, supplemented with uracil, leucine, histidine, lysine, adenine) or YES (0.5% Bacto-yeast extract, 3% glucose, supplemented with uracil, leucine, histidine, lysine, adenine), or YPD (1% Bacto-yeast extract, 2% Bactopeptone, 2% glucose).

**[0053]** The carbon source may, for example, be a sugar such as glucose, fructose or sucrose. The nitrogen source may, for example, be an inorganic acid or an ammonium salt of an inorganic acid, such as ammonia, ammonium chloride or ammonium acetate, peptone or casamino acid. The inorganic salt may, for example, be magnesium phosphate, magnesium sulfate or sodium chloride. Specifically, a nutrient medium such as YPD medium (M.D.Rose et al., "Methods In Yeast Genetics", Cold Spring Harbor Laboratory Press (1990)), a minimal medium such as MB medium (K.Okazaki et al., Nucleic Acids Res., 18, 6485-6489 (1990)) and the like may be used. Cultivation may be carried out by using a publicly known cultivation method for yeasts such as a shaking cultivation, a stirring cultivation.

**[0054]** The cultivation temperature is preferably from 23 to 37°C, more preferably from 30 to 32°C. Further, the cultivation time may be set appropriately.

**[0055]** Cultivation may be carried out by batch culture or continuous culture.

[Method for producing TF]

**[0056]** By culturing a transformant (TF expression strain) using *S. pombe* as a host and having *SP-TF* gene in a liquid medium, TF protein secreted into the liquid medium after culture can be obtained. As the liquid medium for culturing the TF expression strain and the culture method, a publicly known yeast culture medium may be used and a publicly known culture method may be employed, in the same manner as the culture of the transformant of the present invention.

**[0057]** TF protein is easily decomposed under an acidic condition. Accordingly, in production of TF, the pH of the liquid medium for the culture of the TF expression strain is preferably at least 5.5, more preferably from 5.5 to 6.5. The longer the culture time, the more the pH of the culture broth tends to decrease, and accordingly the pH is properly adjusted so that the pH of the culture broth is maintained to be within a range of from 5.5 to 6.5 at the time of the culture for TF production.

**[0058]** In order to further increase the TF protein secretory production amount, the culture time for culturing the TF expression strain is preferably at least 2 days, more preferably from 3 to 6 days, further preferably from 3 to 5 days.

**[0059]** The liquid medium for culturing the TF expression strain preferably contains adenine. In a case where the TF expression strain has the *SP-TF* gene with a copy number of at least one, lysis is likely to occur, and the TF expression amount tends to decrease. By culture in an adenine-containing liquid medium, even a TF expression strain having the *SP-TF* gene with a copy number of at least one favorably grows, thus increasing the TF secretory production efficiency. The adenine content in the liquid medium is, for example, from 0.5 to 200 mg/L, preferably from 1 to 100 mg/L per OD<sub>660</sub> indicating the cell-density.

**[0060]** Further, in order to improve the TF productivity, the TF expression strain is preferably cultured at high density. It is particularly preferred to conduct fed-batch culture using an initial culture medium at a pH of from 5.5 to 6.5, preferably from 5.5 to 6.0 while the aeration rate into a culture tank, the stirring rate and the feeding rate of the feed medium are controlled. Since the medium is continuously added (fed) in accordance with the growth rate and the nutrition consumption rate while the glucose concentration in the medium is kept low at a certain level, the cell-density improves finally several tens times as compared with batch culture in a test tube or in a flask, a high cell-density is achieved, and a larger amount of TF can be produced by secretion. By high concentration culture of the TF expression strain, culture is conducted preferably until OD<sub>660</sub> reaches 100 or higher, preferably OD<sub>660</sub> reaches 200 to 800.

**[0061]** The TF expression strain is preferably the transformant of the present invention. In the transformant of the present invention, Gas2 protein derived from the host is not expressed, and the TF secretory production efficiency is high. In addition, at the time of purification of TF protein from the liquid medium after the high density culture, purification by isolation from Gas2 protein is not necessary, and purification can be carried out more easily.

**[0062]** TF protein can be obtained from the liquid medium after culture by a publicly known method. For example, cells are separated and removed from the liquid medium after culture by centrifugal separation, and the obtained culture supernatant is adsorbed e.g. in an affinity column, followed by washing and elution; impurities such as a dye are removed by activated carbon; or separation may be carried out by using a separation membrane. In a case where the TF expression strain having Gas2 gene is cultured at high density, since the recovered culture supernatant contains Gas2 protein in a large amount, after the culture supernatant is subjected to anion exchange chromatography using a DEAE resin, Gas2 protein is inevitably contained in a fraction containing TF protein. Accordingly, TF protein can be separated and purified from Gas2 protein only after the fraction containing TF protein is subjected to hydrophobic interaction chromatography

or gel permeation chromatography. Whereas from the culture supernatant after the high density culture of the transformant of the present invention, TF protein can be purified only by subjecting the culture supernatant to anion exchange chromatography using a DEAE resin once.

## EXAMPLES

**[0063]** Now, the present invention will be described in further detail with reference to Examples of the present invention and Comparative Examples. However, it should be understood that the present invention is by no means restricted to the following description. In the following Examples, "%" means "mass%" unless otherwise specified.

### [EXAMPLE 1]

#### <Preparation of hTF mutant gene>

**[0064]** A natural *hTF* gene ORF (SEQ ID NO:1) encodes a protein with a full-length of 698 residues, having hTF protein fused to a downstream side of secretion signal peptide having 19 residues. By using human cDNA library as a template, PCR was carried out with a primary pair (forward primer No. 9220 (SEQ ID NO:3) and reverse primer No. 9221 (SEQ ID NO:4)) to obtain a DNA fragment having restriction enzyme site *Afl*III and a nucleotide sequence encoding 4 residues (Leu-Lys-Lys-Arg) of the C-terminal portion of human PDI1 abx-domain at the 5' end of a gene encoding hTF protein, and restriction enzyme site *Xba*I respectively added at the 3' end, respectively.

**[0065]** A double digestion product with *Afl*III and *Xba*I of the DNA fragment obtained was integrated by ligation with a double digestion product with *Afl*III and *Xba*I of pSL6P3 (Patent Document 3) which is a chromosome single-locus integration type secretory expression vector of fission yeast having a gene encoding P3 secretion signal peptide downstream hCMV promoter, and having a multiple cloning site between the gene and LPI terminator, to transform *E. coli* DH5 $\alpha$  to prepare plasmid DNA of expression vector pSL6P3-hTF having a gene encoding natural hTF protein containing 4 residues of the C-terminal portion of abx-domain at the N-terminal cloned.

**[0066]** From a secretory expression vector having an expression cassette of the desired protein integrated into the multiple cloning site of pSL6P3 vector, one copy of a linearized vector fragment cleaved by restriction enzyme *Not*I, is integrated between adjacent two gene loci *leu1-32* and *top2* on the fission yeast chromosome, by chromosome homologous recombination. Further, into pSL6P3 vector, a leucine marker gene fragment (*leu1*<sup>+</sup>) to complement point mutation (*leu1-32*) portion of mutant (*leu1*<sup>-</sup>) gene (a gene having leucine synthesis gene (*leu1*) inactivated by point mutation (*leu1-32*)) is integrated. Accordingly, in a case where a leucine-auxotrophic yeast containing mutant (*leu1*<sup>-</sup>) gene is used as a host strain, the transformant having the linearized fragment of pSL6P3 vector integrated with the chromosome is no more auxotrophic for leucine, and the clone can be selected from the minimal medium (MMA plate) containing no leucine.

**[0067]** By PCR method, into the *hTF* gene in pSL6P3-hTF, a mutation to substitute 413rd and 611st (432nd and 630th of SEQ ID NO:1) aspartic residues of natural hTF protein with glutamic residue was introduced to prepare pSL6P3-hTF(N413Q/N611Q). Specifically, four point mutations to substitute the first nucleotide in the codon encoding each aspartic residue with cytosine (C) and the third nucleotide with adenine (A), were introduced. The sequence of hTF(N413Q/N611Q) having such mutations introduced is shown in SEQ ID NO: 2.

#### <Preparation of hTF(N413Q/N611Q) expression vector>

**[0068]** A DNA fragment containing a region encoding hTF(N413Q/N611Q) having pSL6P3-hTF(N413Q/N611Q) double-digested with *Afl*III and *Xba*I, was integrated by ligation with a double digestion product with *Afl*III and *Xba*I of chromosome single-locus integration type secretory expression vector pSL6PDI1(SP)Hsabx-*Afl*III of fission yeast having a gene encoding secretory carrier protein (PDI1(SP)-Hsabx) comprising a secretion signal peptide of *S. pombe* PDI1, ab-domain of human PDI1 and x-domain of *S. pombe* PDI1, downstream of hCMV promoter, and having a multiple cloning site between the gene and LPI terminator, to transform *E. coli* DH5 $\alpha$  to prepare pSL6PDI1(SP)Hsabx-hTF(N413Q/N611Q) (8749bp, Fig. 1) which is a chromosome single-locus integration type expression vector of a fusion protein of secretory carrier protein (PDI1(SP)-Hsabx) and mutant hTF(N413Q/N611Q) protein.

#### <Preparation of A8 strain>

**[0069]** From leucine/uracil-auxotrophic (*leu1*<sup>-</sup> *ura4*<sup>-</sup>) ARC010 strain (genotype: *h*<sup>-</sup> *leu1-32* *ura4-D18*) of *S. pombe*, by Latour method, eight genes i.e. *psp3* gene, *isp6* gene, *ppp53* gene, *ppp16* gene, *ppp22* gene, *sxa2* gene, *ppp80* gene and *ppp20* gene were deleted to prepare A8 strain (genotype: *h*<sup>-</sup> *leu1-32* *psp3-D13* *isp6-D14* *oma1-D10* *ppp16-D20* *fma2-D13* *sxa2-D15* *aap1-D17* *ppp80-D11*). The A8 strain was a leucine-auxotrophic strain. More particularly, by the

Latour method, a gene deletion fragment (Latour fragment, comprising homologous recombination regions at both terminals, and *ura4<sup>+</sup>* marker gene and OL (overlapped sequence) region sandwiched between the homologous recombination regions), was once integrated by homologous recombination into the upstream or downstream side of the region to be deleted on the fission yeast genome, to prepare a latent strain. Then, the latent strain was cultured in a medium containing 5'-FOA to cause homologous recombination between OLs integrated, to form a gene deletion strain from which the region to be deleted containing *ura4<sup>+</sup>* marker gene dropped off, as a colony. Deletion of the desired gene from the obtained gene deletion strain was confirmed by PCR. By this method, since no foreign gene containing *ura4<sup>+</sup>* marker gene does not remain, only the desired gene can be deleted without integrating a foreign gene, and in addition, deletion of gene can be carried out repeatedly while the *ura4<sup>+</sup>* marker gene is recycled. The nucleotide sequence of the primer used for preparation of the Latour fragment to delete the genes by PCR is shown in Table 1.

TABLE 1

| Gene         | Primer               | Nucleotide sequence        | SEQ ID NO |
|--------------|----------------------|----------------------------|-----------|
| <i>psp3</i>  | Forward primer #6164 | GCAAGTACTGCTCTTGATCTG      | 5         |
|              | Reverse primer #6167 | TAAAGCATCCACTTTGAGCAA      | 6         |
| <i>isp6</i>  | Forward primer #6153 | TCTGTTGGCAACATGTCTC        | 7         |
|              | Reverse primer #6156 | GTGAAAGTAGATTATCCATGAGGTC  | 8         |
| <i>oma1</i>  | Forward primer #7243 | TGCCTTTTACGTTCTTTGGTC      | 9         |
|              | Reverse primer #7246 | TGCACATCAGGTAGCCCGAC       | 10        |
| <i>ppp16</i> | Forward primer #7255 | TCATTAAGTCGTCGTCAAACGG     | 11        |
|              | Reverse primer #7258 | CTTTAGGTCGTCAATTCGTGC      | 12        |
| <i>fma2</i>  | Forward primer #6917 | CATACTCCCCTGATGTTTCGC      | 13        |
|              | Reverse primer #6920 | CATTCATGGTGGTAAGAGTGTTCC   | 14        |
| <i>sxa2</i>  | Forward primer #9515 | ACCAATCTTCCATATCCCCTTG     | 15        |
|              | Reverse primer #9518 | GCTACGAAAGCTTCAACTGCG      | 16        |
| <i>aap1</i>  | Forward primer #9883 | AAAGTTCTTTGTTTTCAATTTCCATG | 17        |
|              | Reverse primer #9886 | TCCTTATAAACGAGCTATCGAATTG  | 18        |
| <i>atg4</i>  | Forward primer #6175 | GAATCATACTACGATCAGTTGC     | 19        |
|              | Reverse primer #6178 | GAAATTTACTCACAGGGAAGAAC    | 20        |

#### <Preparation of A8-gas2Δ strain >

**[0070]** From the A8 strain, *Gas2* gene was deleted by Latour method to prepare A8-gas2Δ strain (genotype: *h<sup>-</sup> leu1-32 psp3-D13 isp6-D14 oma1-D10 ppp16-D20 fma2-D13 sxa2-D15 aap1-D17 ppp80-D11 gas2-D15*). Deletion of the desired gene from the obtained gene deletion strain was confirmed by PCR. The A8-gas2Δ strain was a leucine-auxotrophic strain. The nucleotide sequence of the primer used for preparation of the Latour fragment to delete *Gas2* gene by PCR is shown in Table 2.

TABLE 2

| Gene        | Primer                | Nucleotide sequence         | SEQ ID NO |
|-------------|-----------------------|-----------------------------|-----------|
| <i>gas2</i> | Forward primer #10493 | GAATGTCCATATAAGTCAATGATGAGC | 21        |
|             | Reverse primer #10496 | GAGGTTAACGACTATGGTCTTGTTAAC | 22        |

**[0071]** The prepared A8 strain and A8-gas2Δ strain were subjected to growth evaluation (measurement of  $\mu_{max}$  and growth curve) on a test tube scale (under conditions of inoculation to 5mL of YES and culture at 30°C for 68 hours). As a result, both the strains were confirmed as follows. Although the maximum relative growth rate ( $\mu_{max}$  relative value) indicating the initial rising of cell growth slightly decreased (a decrease of about 8 to 12%) as compared with the same auxotrophic (*leu1<sup>-</sup>*) wild type strain (ARC001), the ultimate cell-density ( $OD_{660}$ ) slightly increased (an increase of about

9 to 17%), and both the strains could grow in the same manner as leucine-auxotrophic wild type strain (not shown). Particularly, no difference in the growth and the phenotype between A8 strain and A8-gas2Δ strain was observed.

#### <Preparation of hTF(N413Q/N611Q) gene one copy expression strain>

**[0072]** pSL6PDI1(SP)Hsabx-hTF(N413Q/N611Q) was cleaved by restriction enzyme *NotI* to prepare a linearized vector fragment (6993 bp), and the vector fragment was integrated by means of lithium acetate method to transform leucine-auxotrophic *S. pombe* A8 strain of A8-gas2Δ strain as a host. Cells after transformation were applied to a MMA plate, and a colony formed by being made to be leucine-auxotrophic, was obtained as a recombinant clone. Then, a clone which was confirmed by PCR that the desired gene was appropriately introduced, was selected as a positive clone (hTF(N413Q/N611Q) expression strain). Transformants having pSL6PDI1(SP)Hsabx-hTF(N413Q/N611Q) introduced into A8 strain and A8-gas2Δ were respectively named A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain.

#### <Secretory production of hTF(N413Q/N611Q) one copy expression strain>

**[0073]** A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain were cultured to express hTF(N413Q/N611Q) by secretion. Specifically, in 5mL of YES in a glass test tube, they were subjected to raising culture and pre-culture respectively for 24 hours, and in 5mL of YPD+MES medium (a liquid medium having 0.3M MES buffer contained in YPD) (pH 6.0) in a glass test tube, shake-cultured at 32°C for 3 days or 5 days. The cell-density at the completion of culture (ultimate OD<sub>660</sub>) was from 30 to 36. The culture supernatant fraction recovered from the culture broth and the cell pellet were respectively subjected to SDS-PAGE analysis and confirmed that hTF(N413Q/N611Q) were expressed inside and outside the cells (not shown). Further, with respect to both A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain, the hTF(N413Q/N611Q) amount in the cell pellet was larger and the hTF(N413Q/N611Q) amount in the culture supernatant was larger in the one cultured for 5 days than in the one cultured for 3 days. Therefore, it was confirmed that by prolonging the culture time, the secretion amount of hTF(N413Q/N611Q) can be increased and the amount remaining in the cells without secretion can be decreased.

#### <Results of hTF(N413Q/N611Q) one copy expression strain>

**[0074]** A8-gas2Δ-hTF(1) strain was cultured to express hTF(N413Q/N611Q) by secretion. Specifically, in 5 mL of YES in a glass test tube, the strain was subjected to raising culture and pre-culture respectively for 24 hours, and then using a 24-well plate, shake-cultured in 5 mL of an adenine-containing YPD+MES medium (pH 6.0) at 32°C for 3 days, 4 days or 5 days, and subjected to ELISA using a commercial kit (tradename: "Human Transferrin ELISA Quantitation Set", manufactured by Bethyl Laboratories), and the hTF(N413Q/N611Q) protein amount secreted into the culture supernatant after completion of the culture was measured. The longer the culture time, the larger the hTF(N413Q/N611Q) secretion amount. The secretion amount of hTF(N413Q/N611Q) per culture supernatant over 5 days of culture was from 30 to 40 mg/L in A8-gas2Δ-hTF(1) strain.

#### <High density culture of hTF(N413Q/N611Q) one copy expression strain>

**[0075]** A8-hTF(1) strain and A8-gas2Δ-hTF(1) strain were cultured at high density to express hTF(N413Q/N611Q) by secretion. Specifically, on a 5L culture scale, fed-batch culture was conducted using an initial culture medium at a pH of the culture broth of from 5.5 to 6.0 while the aeration rate into a culture tank, the stirring rate and the feeding rate of the feed medium were controlled. As the liquid medium, an adenine-containing semisynthetic medium (several % Bacto-yeast extract, synthetic components such as glucose, vitamins, minerals, inorganic salts, etc.) was used. The medium was continuously added (fed) in accordance with the growth rate and the nutrition consumption rate, while the glucose concentration was kept low at 2%. Finally, the cell-density (OD<sub>660</sub>) reached a level of from 200 to 800.

**[0076]** The culture broth was sampled with time and subjected to SDS-PAGE, and the results are shown in Fig. 2. 5 μL of the culture broth was applied to each lane. In Fig. 2, "hTF" indicates a hTF(N413Q/N611Q) band. As shown in the CBB staining image in Fig. 2, expression of gas2 was suppressed in A8-gas2Δ-hTF(1) strain, and the secretion amount of hTF(N413Q/N611Q) in A8-gas2Δ-hTF(1) strain was larger than in A8-hTF(1) strain in all the cases of the culture time of 48, 72 and 96 hours.

**[0077]** Further, ELISA was conducted in the same manner as above using the sampled culture broth, and the hTF(N413Q/N611Q) protein amount secreted into the culture supernatant was measured. As shown in Fig. 3, there was no difference in the secretion amount between the two strains from beginning of the culture up to about 48 hours, however, after about 48 hours, the secretion amount of hTF(N413Q/N611Q) in A8-gas2Δ-hTF(1) strain was definitely larger than in A8-hTF(1) strain. The ultimate secretion amounts of the two strains (secretion amounts 168 hours after beginning of the culture in the case of A8-hTF(1) strain and 96 hours after beginning of the culture in the case of A8-

gas2Δ-hTF(1) strain) are shown in Table 3. Of A8-gas2Δ-hTF(1) strain, the hTF secretion amount per culture broth was at least 4.8 times and the hTF secretion amount per cell (per OD<sub>660</sub>) was at least 2.1 times those of A8-hTF(1) strain.

TABLE 3

| hTF expression         | hTF secretion amount per culture broth (g/L) | hTF secretion amount per cell (mg/OD <sub>660</sub> ) |
|------------------------|--|---|
| A8-hTF(1) strain       | 0.09   | 2.04  |
| A8-gas2Δ-hTF(1) strain | 0.43   | 4.33  |

**[0078]** The cells were removed by centrifugal separation from the culture broth after high density culture, and the recovered culture supernatant was subjected to DEAE chromatography to purify hTF. As the DEAE column, a column packed with a DEAE resin (DEAE Sepharose FF(Fast Flow)) (tradename: "XK26", manufactured by GE Healthcare) was used. Specifically, 900 mL of the culture supernatant was applied to a DEAE column (1 CV=60.6 mL) equilibrated with an equilibration buffer (20 mM Tris-HCl, pH 8.5), and then an elution buffer B (20 mM Tris-HCl, 1M NaCl, pH 8.5) was applied under gradient conditions of from 0% (15 CV) to 100% (5 CV) for elution. The fraction size was 30.3 mL.

**[0079]** Fractions containing hTF(N413Q/N611Q) protein (the 3rd to 6th fractions) were recovered together and subjected to SDS-PAGE, and the results are shown in Fig. 4. In Fig. 4, the lane "after deletion of Gas2" indicates the CBB staining image of the purified fractions from the culture broth of A8-gas2Δ-hTF(1) strain, and the lane "before deletion of Gas2" indicates the CBB staining image of the purified fractions from the culture broth of A8-hTF(1) strain. As shown in the CBB staining images in Fig. 4, in the purified fraction from the culture broth of A8-gas2Δ-hTF(1) strain, only a hTF(N413Q/N611Q) protein band was detected, and it was confirmed that hTF(N413Q/N611Q) protein could be separated from other proteins and purified at high purity only by DEAE chromatography once. Whereas in the purified fraction from the culture broth of A8-hTF(1) strain, in addition to the hTF(N413Q/N611Q) protein band, a plurality of bands were detected at higher molecular weight side. Among them, the band in the vicinity of 115 kDa was taken out and subjected to N terminal sequencing analysis and confirmed to be a Gas2 band. Since secretion of Gas2 was not definitely confirmed by culture at conventional cell-density, it was considered to be characteristic of high density culture. In A8-hTF(1) strain, Gas1 secretory production amount increases in addition to hTF(N413Q/N611Q), which indicates that the hTF(N413Q/N611Q) secretion production amount is kept low as compared with A8-gas2Δ-hTF(1) strain.

**[0080]** The entire disclosure of Japanese Patent Application No. 2016-003606 filed on January 12, 2016 including specification, claims, drawings and summary is incorporated herein by reference in its entirety. (



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|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
|    | TGT | CCA | GGG | TGT | GGC | TGC | TCC | ACC | CTT | AAC | CAA | TAC | TTC | GGC | TAC | TCA | 624  |
|    | Cys | Pro | Gly | Cys | Gly | Cys | Ser | Thr | Leu | Asn | Gln | Tyr | Phe | Gly | Tyr | Ser |      |
|    |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| 5  | GGA | GCC | TTC | AAG | TGT | CTG | AAG | GAT | GGT | GCT | GGG | GAT | GTG | GCC | TTT | GTC | 672  |
|    | Gly | Ala | Phe | Lys | Cys | Leu | Lys | Asp | Gly | Ala | Gly | Asp | Val | Ala | Phe | Val |      |
|    |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
|    | AAG | CAC | TCG | ACT | ATA | TTT | GAG | AAC | TTG | GCA | AAC | AAG | GCT | GAC | AGG | GAC | 720  |
| 10 | Lys | His | Ser | Thr | Ile | Phe | Glu | Asn | Leu | Ala | Asn | Lys | Ala | Asp | Arg | Asp |      |
|    |     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |      |
|    | CAG | TAT | GAG | CTG | CTT | TGC | CTG | GAC | AAC | ACC | CGG | AAG | CCG | GTA | GAT | GAA | 768  |
|    | Gln | Tyr | Glu | Leu | Leu | Cys | Leu | Asp | Asn | Thr | Arg | Lys | Pro | Val | Asp | Glu |      |
|    |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| 15 | TAC | AAG | GAC | TGC | CAC | TTG | GCC | CAG | GTC | CCT | TCT | CAT | ACC | GTC | GTG | GCC | 816  |
|    | Tyr | Lys | Asp | Cys | His | Leu | Ala | Gln | Val | Pro | Ser | His | Thr | Val | Val | Ala |      |
|    |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |      |
|    | CGA | AGT | ATG | GGC | GGC | AAG | GAG | GAC | TTG | ATC | TGG | GAG | CTT | CTC | AAC | CAG | 864  |
| 20 | Arg | Ser | Met | Gly | Gly | Lys | Glu | Asp | Leu | Ile | Trp | Glu | Leu | Leu | Asn | Gln |      |
|    |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
|    | GCC | CAG | GAA | CAT | TTT | GGC | AAA | GAC | AAA | TCA | AAA | GAA | TTC | CAA | CTA | TTC | 912  |
|    | Ala | Gln | Glu | His | Phe | Gly | Lys | Asp | Lys | Ser | Lys | Glu | Phe | Gln | Leu | Phe |      |
|    |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| 25 | AGC | TCT | CCT | CAT | GGG | AAG | GAC | CTG | CTG | TTT | AAG | GAC | TCT | GCC | CAC | GGG | 960  |
|    | Ser | Ser | Pro | His | Gly | Lys | Asp | Leu | Leu | Phe | Lys | Asp | Ser | Ala | His | Gly |      |
|    |     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |      |
|    | TTT | TTA | AAA | GTC | CCC | CCC | AGG | ATG | GAT | GCC | AAG | ATG | TAC | CTG | GGC | TAT | 1008 |
| 30 | Phe | Leu | Lys | Val | Pro | Pro | Arg | Met | Asp | Ala | Lys | Met | Tyr | Leu | Gly | Tyr |      |
|    |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
|    | GAG | TAT | GTC | ACT | GCC | ATC | CGG | AAT | CTA | CGG | GAA | GGC | ACA | TGC | CCA | GAA | 1056 |
|    | Glu | Tyr | Val | Thr | Ala | Ile | Arg | Asn | Leu | Arg | Glu | Gly | Thr | Cys | Pro | Glu |      |
|    |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |      |
| 35 | GCC | CCA | ACA | GAT | GAA | TGC | AAG | CCT | GTG | AAG | TGG | TGT | GCG | CTG | AGC | CAC | 1104 |
|    | Ala | Pro | Thr | Asp | Glu | Cys | Lys | Pro | Val | Lys | Trp | Cys | Ala | Leu | Ser | His |      |
|    |     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |      |
|    | CAC | GAG | AGG | CTC | AAG | TGT | GAT | GAG | TGG | AGT | GTT | AAC | AGT | GTA | GGG | AAA | 1152 |
| 40 | His | Glu | Arg | Leu | Lys | Cys | Asp | Glu | Trp | Ser | Val | Asn | Ser | Val | Gly | Lys |      |
|    |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
|    | ATA | GAG | TGT | GTA | TCA | GCA | GAG | ACC | ACC | GAA | GAC | TGC | ATC | GCC | AAG | ATC | 1200 |
|    | Ile | Glu | Cys | Val | Ser | Ala | Glu | Thr | Thr | Glu | Asp | Cys | Ile | Ala | Lys | Ile |      |
|    |     |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |      |
| 45 | ATG | AAT | GGA | GAA | GCT | GAT | GCC | ATG | AGC | TTG | GAT | GGA | GGG | TTT | GTC | TAC | 1248 |
|    | Met | Asn | Gly | Glu | Ala | Asp | Ala | Met | Ser | Leu | Asp | Gly | Gly | Phe | Val | Tyr |      |
|    |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |      |
|    | ATA | GCG | GGC | AAG | TGT | GGT | CTG | GTG | CCT | GTC | TTG | GCA | GAA | AAC | TAC | AAT | 1296 |
| 50 | Ile | Ala | Gly | Lys | Cys | Gly | Leu | Val | Pro | Val | Leu | Ala | Glu | Asn | Tyr | Asn |      |
|    |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |      |
|    | AAG | AGC | GAT | AAT | TGT | GAG | GAT | ACA | CCA | GAG | GCA | GGG | TAT | TTT | GCT | GTA | 1344 |
|    | Lys | Ser | Asp | Asn | Cys | Glu | Asp | Thr | Pro | Glu | Ala | Gly | Tyr | Phe | Ala | Val |      |
|    |     |     | 435 |     |     |     |     | 440 |     |     |     | 445 |     |     |     |     |      |
| 55 | GCA | GTG | GTG | AAG | AAA | TCA | GCT | TCT | GAC | CTC | ACC | TGG | GAC | AAT | CTG | AAA | 1392 |
|    | Ala | Val | Val | Lys | Lys | Ser | Ala | Ser | Asp | Leu | Thr | Trp | Asp | Asn | Leu | Lys |      |
|    |     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |

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5 GGC AAG AAG TCC TGC CAT ACG GCA GTT GGC AGA ACC GCT GGC TGG AAC 1440  
 Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn  
 465 470 475 480  
 10 ATC CCC ATG GGC CTG CTC TAC AAT AAG ATC AAC CAC TGC AGA TTT GAT 1488  
 Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp  
 485 490 495  
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 Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser  
 500 505 510  
 20 CTC TGT AAG CTG TGT ATG GGC TCA GGC CTA AAC CTG TGT GAA CCC AAC 1584  
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 515 520 525  
 25 AAC AAA GAG GGA TAC TAC GGC TAC ACA GGC GCT TTC AGG TGT CTG GTT 1632  
 Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val  
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 30 GAG AAG GGA GAT GTG GCC TTT GTG AAA CAC CAG ACT GTC CCA CAG AAC 1680  
 Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn  
 545 550 555 560  
 35 ACT GGG GGA AAA AAC CCT GAT CCA TGG GCT AAG AAT CTG AAT GAA AAA 1728  
 Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys  
 565 570 575  
 40 GAC TAT GAG TTG CTG TGC CTT GAT GGT ACC AGG AAA CCT GTG GAG GAG 1776  
 Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu  
 580 585 590  
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 Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr  
 595 600 605  
 50 CGG AAA GAT AAG GAA GCT TGC GTC CAC AAG ATA TTA CGT CAA CAG CAG 1872  
 Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln  
 610 615 620  
 55 CAC CTA TTT GGA AGC AAC GTA ACT GAC TGC TCG GGC AAC TTT TGT TTG 1920  
 His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu  
 625 630 635 640  
 60 TTC CGG TCG GAA ACC AAG GAC CTT CTG TTC AGA GAT GAC ACA GTA TGT 1968  
 Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys  
 645 650 655  
 65 TTG GCC AAA CTT CAT GAC AGA AAC ACA TAT GAA AAA TAC TTA GGA GAA 2016  
 Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu  
 660 665 670  
 70 GAA TAT GTC AAG GCT GTT GGT AAC CTG AGA AAA TGC TCC ACC TCA TCA 2064  
 Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser  
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 690 695

<210> 2

<211> 2040

<212> DNA

<213> Homo sapiens

<220>

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<223> mutant of transferrin (N413Q/N611Q)

<400> 2

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|    | Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala |     |
|    | 5 10 15   |     |
|    | ACT AAG TGC CAG AGT TTC CGC GAC CAT ATG AAA AGC GTC ATT CCA TCC | 96  |
|    | Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser |     |
|    | 20 25 30  |     |
| 10 | GAT GGT CCC AGT GTT GCT TGT GTG AAG AAA GCC TCC TAC CTT GAT TGC | 144 |
|    | Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys |     |
|    | 35 40 45  |     |
|    | ATC AGG GCC ATT GCG GCA AAC GAA GCG GAT GCT GTG ACA CTG GAT GCA | 192 |
| 15 | Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala |     |
|    | 50 55 60  |     |
|    | GGT TTG GTG TAT GAT GCT TAC CTG GCT CCC AAT AAC CTG AAG CCT GTG | 240 |
|    | Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val |     |
|    | 65 70 75 80   |     |
| 20 | GTG GCA GAG TTC TAT GGG TCA AAA GAG GAT CCA CAG ACT TTC TAT TAT | 288 |
|    | Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr |     |
|    | 85 90 95  |     |
|    | GCT GTT GCT GTG GTG AAG AAG GAT AGT GGC TTC CAG ATG AAC CAG CTT | 336 |
| 25 | Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu |     |
|    | 100 105 110   |     |
|    | CGA GGC AAG AAG TCC TGC CAC ACG GGT CTA GGC AGG TCC GCT GGG TGG | 384 |
|    | Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp |     |
|    | 115 120 125   |     |
| 30 | AAC ATC CCC ATA GGC TTA CTT TAC TGT GAC TTA CCT GAG CCA CGT AAA | 432 |
|    | Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys |     |
|    | 130 135 140   |     |
|    | CCT CTT GAG AAA GCA GTG GCC AAT TTC TTC TCG GGC AGC TGT GCC CCT | 480 |
| 35 | Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro |     |
|    | 145 150 155 160   |     |
|    | TGT GCG GAT GGG ACG GAC TTC CCC CAG CTG TGT CAA CTG TGT CCA GGG | 528 |
|    | Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu Cys Pro Gly |     |
|    | 165 170 175   |     |
| 40 | TGT GGC TGC TCC ACC CTT AAC CAA TAC TTC GGC TAC TCA GGA GCC TTC | 576 |
|    | Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser Gly Ala Phe |     |
|    | 180 185 190   |     |
|    | AAG TGT CTG AAG GAT GGT GCT GGG GAT GTG GCC TTT GTC AAG CAC TCG | 624 |
| 45 | Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val Lys His Ser |     |
|    | 195 200 205   |     |
|    | ACT ATA TTT GAG AAC TTG GCA AAC AAG GCT GAC AGG GAC CAG TAT GAG | 672 |
|    | Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp Gln Tyr Glu |     |
|    | 210 215 220   |     |
| 50 | CTG CTT TGC CTG GAC AAC ACC CGG AAG CCG GTA GAT GAA TAC AAG GAC | 720 |
|    | Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu Tyr Lys Asp |     |
|    | 225 230 235 240   |     |
|    | TGC CAC TTG GCC CAG GTC CCT TCT CAT ACC GTC GTG GCC CGA AGT ATG | 768 |
| 55 | Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala Arg Ser Met |     |
|    | 245 250 255   |     |
|    | GGC GGC AAG GAG GAC TTG ATC TGG GAG CTT CTC AAC CAG GCC CAG GAA | 816 |

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|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
|    | Gly | Gly | Lys | Glu | Asp | Leu | Ile | Trp | Glu | Leu | Leu | Asn | Gln | Ala | Gln | Glu |      |
|    |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| 5  | CAT | TTT | GGC | AAA | GAC | AAA | TCA | AAA | GAA | TTC | CAA | CTA | TTC | AGC | TCT | CCT | 864  |
|    | His | Phe | Gly | Lys | Asp | Lys | Ser | Lys | Glu | Phe | Gln | Leu | Phe | Ser | Ser | Pro |      |
|    |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
|    | CAT | GGG | AAG | GAC | CTG | CTG | TTT | AAG | GAC | TCT | GCC | CAC | GGG | TTT | TTA | AAA | 912  |
|    | His | Gly | Lys | Asp | Leu | Leu | Phe | Lys | Asp | Ser | Ala | His | Gly | Phe | Leu | Lys |      |
| 10 |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |      |
|    | GTC | CCC | CCC | AGG | ATG | GAT | GCC | AAG | ATG | TAC | CTG | GGC | TAT | GAG | TAT | GTC | 960  |
|    | Val | Pro | Pro | Arg | Met | Asp | Ala | Lys | Met | Tyr | Leu | Gly | Tyr | Glu | Tyr | Val |      |
|    |     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |      |
|    | ACT | GCC | ATC | CGG | AAT | CTA | CGG | GAA | GGC | ACA | TGC | CCA | GAA | GCC | CCA | ACA | 1008 |
| 15 | Thr | Ala | Ile | Arg | Asn | Leu | Arg | Glu | Gly | Thr | Cys | Pro | Glu | Ala | Pro | Thr |      |
|    |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |      |
|    | GAT | GAA | TGC | AAG | CCT | GTG | AAG | TGG | TGT | GCG | CTG | AGC | CAC | CAC | GAG | AGG | 1056 |
|    | Asp | Glu | Cys | Lys | Pro | Val | Lys | Trp | Cys | Ala | Leu | Ser | His | His | Glu | Arg |      |
|    |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |      |
| 20 | CTC | AAG | TGT | GAT | GAG | TGG | AGT | GTT | AAC | AGT | GTA | GGG | AAA | ATA | GAG | TGT | 1104 |
|    | Leu | Lys | Cys | Asp | Glu | Trp | Ser | Val | Asn | Ser | Val | Gly | Lys | Ile | Glu | Cys |      |
|    |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
|    | GTA | TCA | GCA | GAG | ACC | ACC | GAA | GAC | TGC | ATC | GCC | AAG | ATC | ATG | AAT | GGA | 1152 |
| 25 | Val | Ser | Ala | Glu | Thr | Thr | Glu | Asp | Cys | Ile | Ala | Lys | Ile | Met | Asn | Gly |      |
|    |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
|    | GAA | GCT | GAT | GCC | ATG | AGC | TTG | GAT | GGA | GGG | TTT | GTC | TAC | ATA | GCG | GGC | 1200 |
|    | Glu | Ala | Asp | Ala | Met | Ser | Leu | Asp | Gly | Gly | Phe | Val | Tyr | Ile | Ala | Gly |      |
|    |     |     | 385 |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |      |
| 30 | AAG | TGT | GGT | CTG | GTG | CCT | GTC | TTG | GCA | GAA | AAC | TAC | CAA | AAG | AGC | GAT | 1248 |
|    | Lys | Cys | Gly | Leu | Val | Pro | Val | Leu | Ala | Glu | Asn | Tyr | Gln | Lys | Ser | Asp |      |
|    |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |      |
|    | AAT | TGT | GAG | GAT | ACA | CCA | GAG | GCA | GGG | TAT | TTT | GCT | GTA | GCA | GTG | GTG | 1296 |
| 35 | Asn | Cys | Glu | Asp | Thr | Pro | Glu | Ala | Gly | Tyr | Phe | Ala | Val | Ala | Val | Val |      |
|    |     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |     |      |
|    | AAG | AAA | TCA | GCT | TCT | GAC | CTC | ACC | TGG | GAC | AAT | CTG | AAA | GGC | AAG | AAG | 1344 |
|    | Lys | Lys | Ser | Ala | Ser | Asp | Leu | Thr | Trp | Asp | Asn | Leu | Lys | Gly | Lys | Lys |      |
|    |     |     | 435 |     |     |     |     | 440 |     |     |     | 445 |     |     |     |     |      |
| 40 | TCC | TGC | CAT | ACG | GCA | GTT | GGC | AGA | ACC | GCT | GGC | TGG | AAC | ATC | CCC | ATG | 1392 |
|    | Ser | Cys | His | Thr | Ala | Val | Gly | Arg | Thr | Ala | Gly | Trp | Asn | Ile | Pro | Met |      |
|    |     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
|    | GGC | CTG | CTC | TAC | AAT | AAG | ATC | AAC | CAC | TGC | AGA | TTT | GAT | GAA | TTT | TTC | 1440 |
| 45 | Gly | Leu | Leu | Tyr | Asn | Lys | Ile | Asn | His | Cys | Arg | Phe | Asp | Glu | Phe | Phe |      |
|    |     |     | 465 |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |      |
|    | AGT | GAA | GGT | TGT | GCC | CCT | GGG | TCT | AAG | AAA | GAC | TCC | AGT | CTC | TGT | AAG | 1488 |
|    | Ser | Glu | Gly | Cys | Ala | Pro | Gly | Ser | Lys | Lys | Asp | Ser | Ser | Leu | Cys | Lys |      |
|    |     |     |     | 485 |     |     |     |     |     | 490 |     |     |     | 495 |     |     |      |
| 50 | CTG | TGT | ATG | GGC | TCA | GGC | CTA | AAC | CTG | TGT | GAA | CCC | AAC | AAC | AAA | GAG | 1536 |
|    | Leu | Cys | Met | Gly | Ser | Gly | Leu | Asn | Leu | Cys | Glu | Pro | Asn | Asn | Lys | Glu |      |
|    |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |      |
|    | GGA | TAC | TAC | GGC | TAC | ACA | GGC | GCT | TTC | AGG | TGT | CTG | GTT | GAG | AAG | GGA | 1584 |
| 55 | Gly | Tyr | Tyr | Gly | Tyr | Thr | Gly | Ala | Phe | Arg | Cys | Leu | Val | Glu | Lys | Gly |      |
|    |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
|    | GAT | GTG | GCC | TTT | GTG | AAA | CAC | CAG | ACT | GTC | CCA | CAG | AAC | ACT | GGG | GGA | 1632 |

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|    |  |      |
|----|--|------|
|    | Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly  |      |
|    | 530 535 540  |      |
| 5  | AAA AAC CCT GAT CCA TGG GCT AAG AAT CTG AAT GAA AAA GAC TAT GAG<br>Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu | 1680 |
|    | 545 550 555 560  |      |
|    | TTG CTG TGC CTT GAT GGT ACC AGG AAA CCT GTG GAG GAG TAT GCG AAC<br>Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn | 1728 |
|    | 565 570 575  |      |
| 10 | TGC CAC CTG GCC AGA GCC CCG AAT CAC GCT GTG GTC ACA CGG AAA GAT<br>Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr Arg Lys Asp | 1776 |
|    | 580 585 590  |      |
| 15 | AAG GAA GCT TGC GTC CAC AAG ATA TTA CGT CAA CAG CAG CAC CTA TTT<br>Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe | 1824 |
|    | 595 600 605  |      |
|    | GGA AGC CAA GTA ACT GAC TGC TCG GGC AAC TTT TGT TTG TTC CGG TCG<br>Gly Ser Gln Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser | 1872 |
|    | 610 615 620  |      |
| 20 | GAA ACC AAG GAC CTT CTG TTC AGA GAT GAC ACA GTA TGT TTG GCC AAA<br>Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys | 1920 |
|    | 625 630 635 640  |      |
|    | CTT CAT GAC AGA AAC ACA TAT GAA AAA TAC TTA GGA GAA GAA TAT GTC<br>Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val | 1968 |
| 25 | 645 650 655  |      |
|    | AAG GCT GTT GGT AAC CTG AGA AAA TGC TCC ACC TCA TCA CTC CTG GAA<br>Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu | 2016 |
|    | 660 665 670  |      |
| 30 | GCC TGC ACT TTC CGT AGA CCT TAA<br>Ala Cys Thr Phe Arg Arg Pro   | 2040 |
|    | 675  |      |
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| 55 | <210> 5<br><211> 21  |      |

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|----|--|----|
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|    | <213> Artificial Sequence                                      |    |
|    | <220>  |    |
| 5  | <223> Description of Artificial Sequence: Forward primer #6164 |    |
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|    | <210> 6  |    |
| 10 | <211> 21   |    |
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|    | <213> Artificial Sequence                                      |    |
|    | <220>  |    |
| 15 | <223> Description of Artificial Sequence: Reverse primer #6167 |    |
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|    | <210> 7  |    |
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|    | <213> Artificial Sequence                                      |    |
|    | <220>  |    |
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|    | <210> 8  |    |
| 30 | <211> 25   |    |
|    | <212> DNA  |    |
|    | <213> Artificial Sequence                                      |    |
|    | <220>  |    |
| 35 | <223> Description of Artificial Sequence: Reverse primer #6156 |    |
|    | <400> 8  |    |
|    | gtgaaagtag attatccatg aggtc                                    | 25 |
|    | <210> 9  |    |
| 40 | <211> 22   |    |
|    | <212> DNA  |    |
|    | <213> Artificial Sequence                                      |    |
|    | <220>  |    |
| 45 | <223> Description of Artificial Sequence: Forward primer #7243 |    |
|    | <400> 9  |    |
|    | tgcccttttac ggttcttttg tc                                      | 22 |
|    | <210> 10   |    |
| 50 | <211> 20   |    |
|    | <212> DNA  |    |
|    | <213> Artificial Sequence                                      |    |
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| 55 | <223> Description of Artificial Sequence: Reverse primer #7246 |    |
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|    |   |    |
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| 5  | <210> 17  |    |
|    | <211> 26  |    |
|    | <212> DNA   |    |
|    | <213> Artificial Sequence                                       |    |
| 10 | <220>   |    |
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|    | <211> 25  |    |
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|    | <213> Artificial Sequence                                       |    |
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|    | <213> Artificial Sequence                                       |    |
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| 35 | <210> 20  |    |
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|    | <212> DNA   |    |
|    | <213> Artificial Sequence                                       |    |
| 40 | <220>   |    |
|    | <223> Description of Artificial Sequence: Reverse primer #6178  |    |
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| 45 | <210> 21  |    |
|    | <211> 27  |    |
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|    | <213> Artificial Sequence                                       |    |
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| 55 | <210> 22  |    |
|    | <211> 27  |    |

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<223> Description of Artificial Sequence: Reverse primer #10496

<400> 22

gaggttaacg actatggtct tgtaaac

27

## Claims

1. A transformant using *Schizosaccharomyces pombe* as a host, comprising a transferrin gene and a secretion signal peptide gene expressing transferrin to which a secretion signal peptide which functions in the host binds, located in an upstream region of the transferrin gene, and having Gas2 gene endogenous to the host deleted or inactivated.
2. The transformant according to Claim 1, wherein the transferrin gene is a gene encoding natural TF protein derived from a mammal, or its modified protein.
3. The transformant according to Claim 1 or 2, wherein the transferrin gene is a gene encoding human transferrin or its modified protein.
4. The transformant according to Claim 1 or 2, wherein the transferrin gene is a mutant transferrin gene having a mutation introduced to a gene encoding natural mammal transferrin, and the mutant transferrin gene is a gene encoding mutant transferrin having at least one aspartic residue which is a N-linked glycosylated portion of natural transferrin deleted or substituted with another amino acid residue.
5. The transformant according to Claim 4, wherein the transferrin gene is a mutant transferrin gene having a mutation introduced to a gene encoding natural human transferrin.
6. The transformant according to any one of Claims 1 to 5, wherein at least one protease gene endogenous to the host is deleted or inactivated.
7. The transformant according to Claim 6, wherein the protease gene is a gene selected from the group consisting of a metalloproteinase gene group, a serine protease gene group, a cysteine protease gene group and an aspartic protease gene group.
8. The transformant according to Claim 6 or 7, wherein the protease gene is a gene selected from the group consisting of psp3 gene, isp6 gene, ppp53 gene, ppp16 gene, ppp22 gene, sxa2 gene, ppp80 gene and ppp20 gene.
9. The transformant according to any one of Claims 1 to 8, wherein the transferrin gene is located downstream of a gene encoding a secretory carrier protein containing a secretion signal peptide, directly or indirectly.
10. The transformant according Claim 9, wherein the gene encoding a secretory carrier protein is a fusion gene of a gene encoding a secretion signal peptide portion of host PDI1, a gene encoding an ab-domain portion of human PDI1, and a gene encoding an x-domain portion of host PDI1.
11. A method for producing transferrin, which comprises culturing the transformant as defined in any one of Claims 1 to 10 in a liquid medium and obtaining transferrin from the liquid medium.
12. The method for producing transferrin according to Claim 11, wherein the transformant is cultured in a liquid medium having a pH of from 5.5 to 6.5.
13. The method for producing transferrin according to Claim 11 or 12, wherein the transformant is cultured in a liquid medium containing adenine.
14. The method for producing transferrin according to any one of Claims 11 to 13, wherein the transformant is cultured until the cell-density ( $OD_{660}$ ) reaches 100 or higher, and then transferrin is obtained from the liquid medium.

15. A method for producing a transformant, which comprises integrating into *Schizosaccharomyces pombe* as a host, a secretion signal peptide gene which functions in the host, and a transferrin gene located downstream of the secretion signal peptide gene, and deleting or inactivating Gas2 gene endogenous to the host.

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Fig. 1

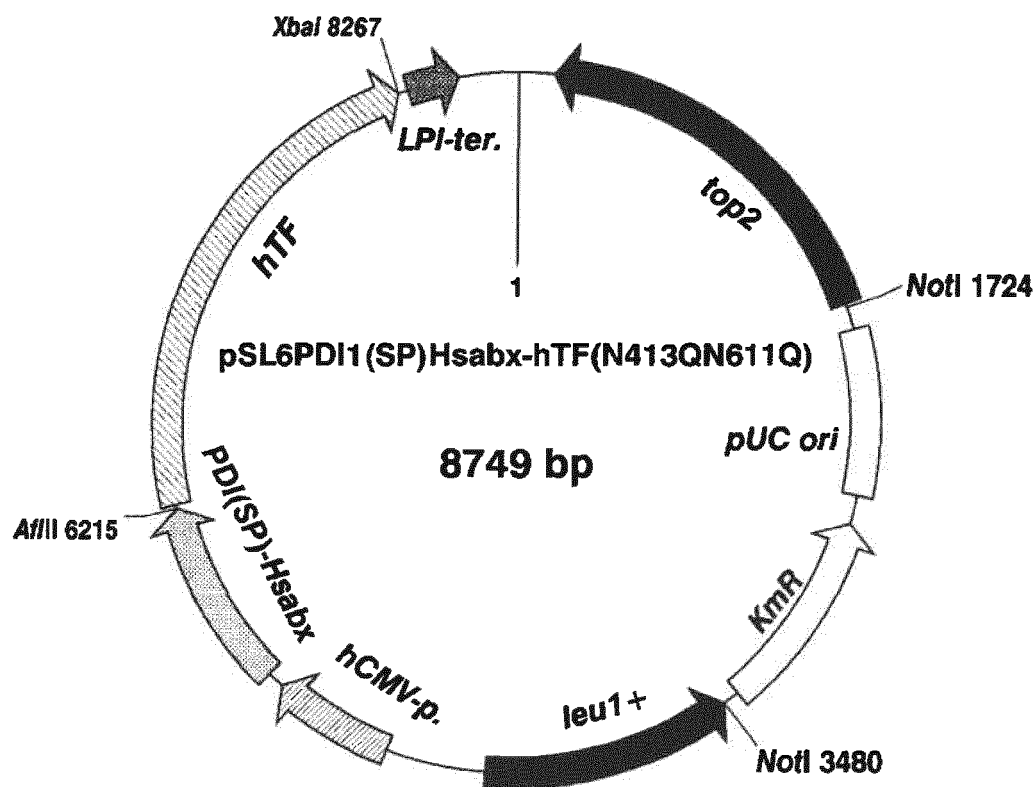


Fig. 2

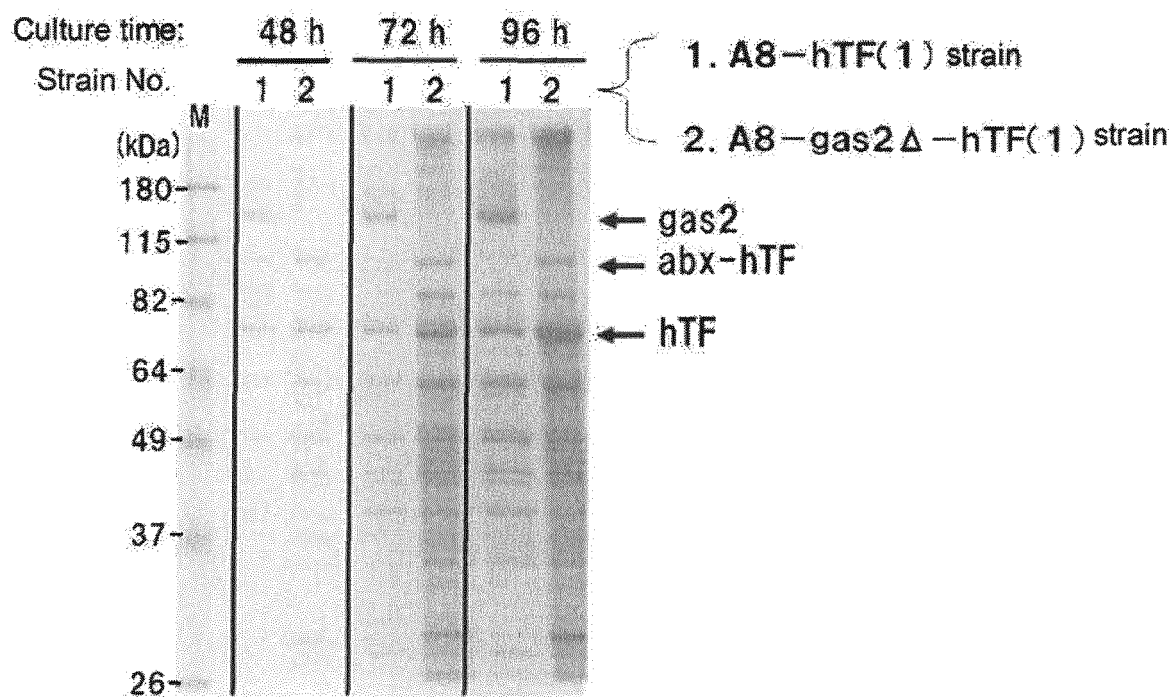


Fig. 3

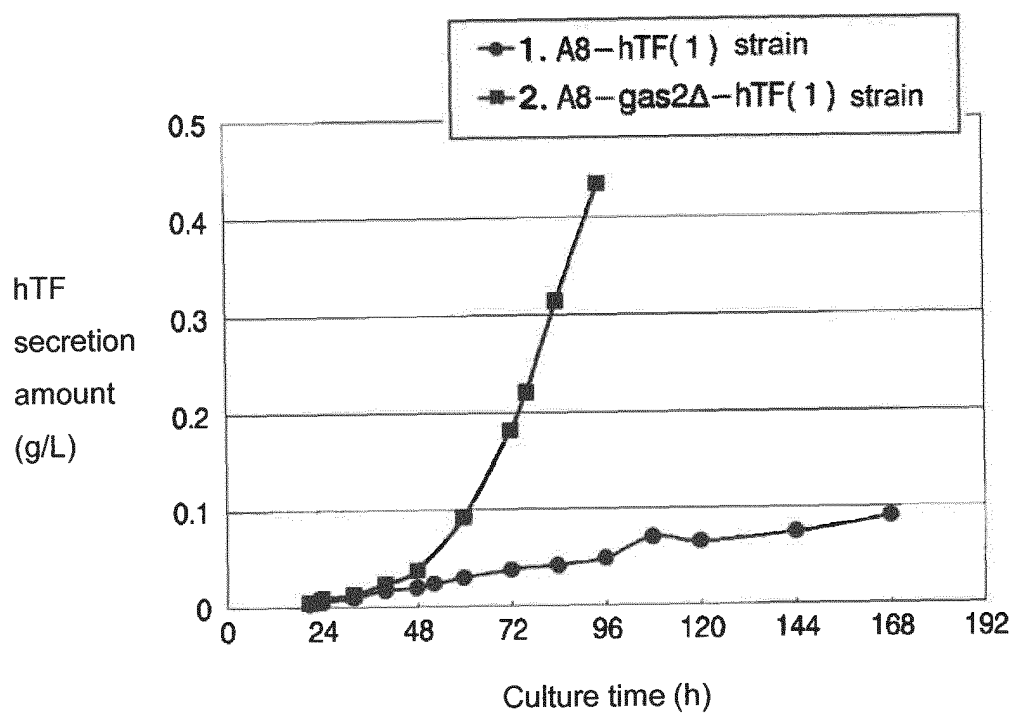
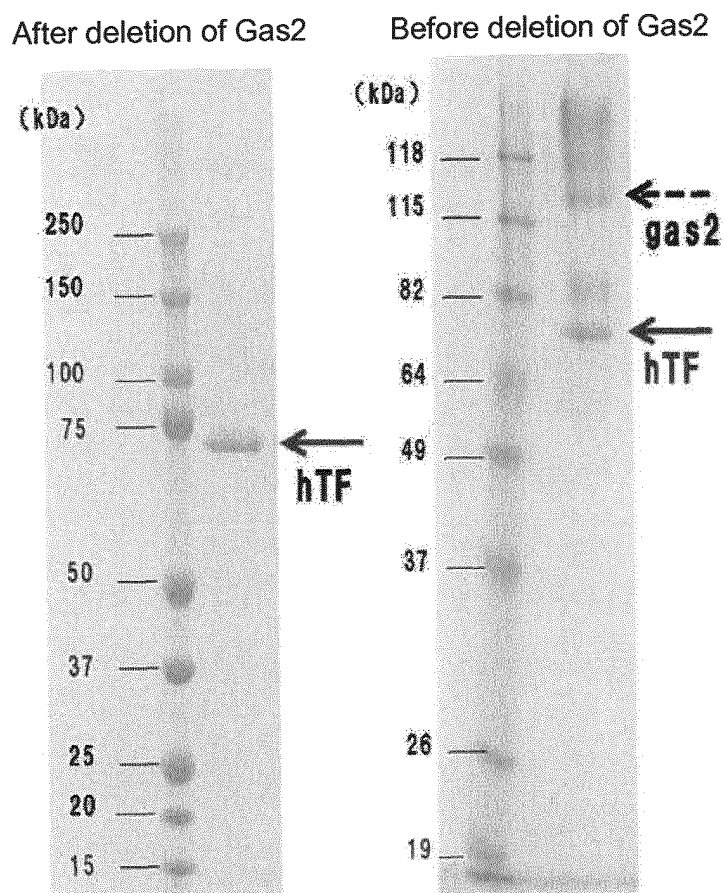


Fig. 4



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2017/000497

## A. CLASSIFICATION OF SUBJECT MATTER

C12N15/09(2006.01)i, C12N1/19(2006.01)i, C12P21/00(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N15/09, C12N1/19, C12P21/00

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

|                           |           |                            |           |
|---------------------------|-----------|----------------------------|-----------|
| Jitsuyo Shinan Koho       | 1922-1996 | Jitsuyo Shinan Toroku Koho | 1996-2017 |
| Kokai Jitsuyo Shinan Koho | 1971-2017 | Toroku Jitsuyo Shinan Koho | 1994-2017 |

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

JSTPlus/JMEDPlus/JST7580(JDREAMIII), CAPLUS/MEDLINE/EMBASE/BIOSIS(STN)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages  | Relevant to claim No. |
|-----------|---|-----------------------|
| A         | WO 2007/015470 A1 (Asahi Glass Co., Ltd.),<br>08 February 2007 (08.02.2007),<br>claims; paragraphs [0009], [0010]<br>& US 2008/0206816 A1<br>claims; paragraphs [0021], [0022]<br>& US 2013/0122547 A1 & EP 1930428 A1<br>& EP 2182060 A1 & CA 2617832 A<br>& JP 2007-529263 A & JP 2010-220626 A<br>& JP 5131457 B2 & JP 513493 B2 | 1-15                  |
| A         | JP 2011-125281 A (Asahi Glass Co., Ltd.),<br>30 June 2011 (30.06.2011),<br>claims<br>(Family: none)   | 1-15                  |

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&amp;" document member of the same patent family

Date of the actual completion of the international search  
16 March 2017 (16.03.17)Date of mailing of the international search report  
04 April 2017 (04.04.17)Name and mailing address of the ISA/  
Japan Patent Office  
3-4-3, Kasumigaseki, Chiyoda-ku,  
Tokyo 100-8915, Japan

Authorized officer

Telephone No.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2017/000497

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages  | Relevant to claim No. |
|-----------|---|-----------------------|
| A         | DE MEDINA-REDONDO, M. et al., $\beta(1,3)$ -Glucanosyl-Transferase Activity Is Essential for Cell Wall Integrity and Viability of <i>Scyzosaccharomyces pombe</i> , PLoS ONE, 2010, Vol.5, e14046 | 1-15                  |

Form PCT/ISA/210 (continuation of second sheet) (January 2015)

## REFERENCES CITED IN THE DESCRIPTION

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